WEST Search History

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DATE: Monday, April 11, 2005

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☐	L23	L22 and l11	7
☐	L22	west$3 adj nile and ("3'-non-coding" or "3'-noncoding" or "3'" adj (non-coding or noncoding))	244
☐	L21	west$3 adj nile with ("3'-non-coding" or "3'-noncoding" or "3'" adj (non-coding or noncoding))	2
☐	L20	(probe or primer or amplif$ or hybridiz$) and west$3 adj nile same ("3'-non-coding" or "3'-noncoding" or "3'" adj (non-coding or noncoding))	3
☐	L19	L18 and (L11 or L16)	16
☐	L18	west$3 adj nile with (NS5 or ns-5 or (nonstructural or non-structural) near4 5)	16
☐	L17	L16 and L11	18
☐	L16	(probe or primer or amplif$ or hybridiz$) and west$3 adj nile same (NS5 or ns-5 or (nonstructural or non-structural) near4 5)	24
☐	L15	L13 and west adj nile	37
☐	L14	L6 and L3 not L4	8
☐	L13	L11 and (probe or primer or amplif$) same (diagnos$ or detect$ or determin$ or identif$) with virus	77
☐	L12	(probe or primer) with ($3PCR or polymerase adj chain adj reaction or hybridiz$) same (flavivirus or japanese adj encephalitis or west adj nile)	69
☐	L11	(probe or primer) same (flavivirus or japanese adj encephalitis or west adj nile)	107
☐	L10	L9 and (diagnos$ or detect$ or determin$ or identif$) with virus	19
☐	L9	L8 and L3	49
☐	L8	L7 and L4	81
☐	L7	L6 and L1	92
☐	L6	primer with promot$5 with polymerase	2386
☐	L5	L4 and L3	109
☐	L4	20021016	196
☐	L3	L1 and ($3PCR or hybridiz$) with (detect or determin$)	128
☐	L2	L1 and ($3PCR or hybridiz$) with (detect or determin$) same (Flavivirus or Japanese adj encephalitis or West adj Nile or virus)	4
☐	L1	primer same (promotor or control) with ("T7" or RNA) near2 polymerase	237

END OF SEARCH HISTORY

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Field: **Title/Abstract**

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- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#28	Search **"West Nile" AND genome[ti]** Field: **Title/Abstract**	13:56:25	20
#24	**Related Articles** for **PubMed** (Select **9158052**)	13:45:32	294
#22	Search **("West Nile" or "Western Nile") AND virus AND ("3'" AND (non-coding or noncoding) or "3'-noncoding" or "3'-non-coding")** Field: **Title/Abstract**	13:44:57	13
#15	Search **#14 AND NS5** Field: **Title/Abstract**	13:18:17	23
#14	Search **("West Nile" or "Western Nile") AND virus AND (NS5 or nonstructural or non-structural)** Field: **Title/Abstract**	12:48:25	59

Clear History

STN

FILE 'HOME' ENTERED AT 13:22:41 ON 11 APR 2005

L1 732 (WEST (A) NILE) (S) VIRUS AND (RT-PCR OR PCR OR POLYMERASE (A) (CHAIN (A) REACTION OR CHAIN-REACTION) OR PRIMER? OR HYBRIDIZ?)

L2 151 WEST (A) NILE AND (NS5 OR (NON-STRUCTURAL OR NONSTRUCTURAL) (S) "5")

(FILE 'HOME' ENTERED AT 13:22:41 ON 11 APR 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 13:22:59 ON 11 APR 2005

L1 732 S (WEST (A) NILE) (S) VIRUS AND (RT-PCR OR PCR OR POLYMERASE (A
L2 151 S WEST (A) NILE AND (NS5 OR (NON-STRUCTURAL OR NONSTRUCTURAL) (
L3 52 S L1 AND L2
L4 21 S L1 AND "3'" (S)(NON-CODING OR NONCODING)
L5 7 DUP REM L4 (14 DUPLICATES REMOVED)
L6 20 DUP REM L3 (32 DUPLICATES REMOVED)
L7 11 S L6 AND PY<2003

L5 ANSWER 1 OF 7 MEDLINE on STN DUPLICATE 1
AN 2004065831 MEDLINE
DN PubMed ID: 14766868
TI Use of an internal positive control in a multiplex reverse transcription-**PCR** to detect **West Nile virus** RNA in mosquito pools.
AU Eisler Diane L; McNabb Alan; Jorgensen Danielle R; Isaac-Renton Judith L
CS Division of Laboratory Services, British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada.. diane.eisler@bccdc.ca
SO Journal of clinical microbiology, (2004 Feb) 42 (2) 841-3. Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF196835
EM 200404
ED Entered STN: 20040210
Last Updated on STN: 20040410
Entered Medline: 20040409
AB We report on the use of **West Nile virus** Armored RNA as an internal positive control (IPC) for the extraction and reverse transcription-**PCR** (**RT-PCR**) of RNA extracted from field-collected mosquitoes and on a multiplex real-time Taqman **RT-PCR** to simultaneously detect the **3** ' **noncoding** region of **West Nile virus** and the **West Nile virus** NS5-2 region comprising the IPC. Mosquito pools from the province of British Columbia, Canada (n = 635), were tested in duplicate and found to be negative for **West Nile virus** and positive for the IPC. Known **West Nile virus**-positive supernatants from mosquito pools from the provinces of Alberta and Manitoba were tested in duplicate and found to be positive for both regions of the **West Nile virus** genome. The mean cycle threshold (Ct) value for the IPC in batch extraction controls +/- 2 standard deviations was found to be 36.43 +/- 1.78 cycles. IPCs of 98.4% (624) of **West Nile virus**-negative pools fell within this range, indicating the reproducibility of RNA extraction and **RT-PCR** for pools varying in mosquito genus and number. A comparison of mosquito pool genera revealed no significant genus effect on the Ct value of the IPC. The incorporation of **West Nile virus** Armored RNA as an IPC allows monitoring of RNA extraction and **RT-PCR** and detection of false-negative results due to failures in these processes or to **PCR** inhibition, respectively.

L5 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:842060 CAPLUS
DN 138:148319
TI Rapid detection of **West Nile Virus**
AU Landt, Olfert; Dehnhardt, Jasmin; Nitsche, Andreas; Milburn, Gary; Carver, Shawn D.
CS Research and Development Unit, TIB MOLBIOL Berlin, Berlin, 10829, Germany
SO Rapid Cycle Real-Time PCR: Methods and Applications--Microbiology and Food Analysis (2002), 227-234. Editor(s): Reischl, Udo; Wittwer, Carl; Cockerill, Franklin. Publisher: Springer-Verlag, Berlin, Germany. CODEN: 69DFMB; ISBN: 3-540-41881-4
DT Conference
LA English
AB **West Nile virus** (WNV) is a flavivirus endemic in Africa, the Middle East, and in South-Western Asia. The virus is a member of the Japanese encephalitis serocomplex, containing a plus-strand ssRNA genome. A few **RT-PCR** based diagnostic assays have been previously described. The amplification efficiency and detection are usually based on the TaqMan probe based real-time **PCR** assays using the genomic region for the nonstructural proteins NS3 and NS5. The developed rapid method uses a new **hybridization**

probe-based assay targeting the published **3'-noncoding** region (3NC sequences).

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2001:781171 CAPLUS
DN 135:340146
TI Flavivirus detection and quantification assay using fluorogenic **RT -PCR**
IN Houng, Huo-Shu H.; Kanesa-Thasan, Niranjan
PA U.S. Army Medical Research and Material Command, USA
SO PCT Int. Appl., 50 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001079546	A2	20011025	WO 2000-US28961	20001019
WO 2001079546	A3	20030605		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6793488	B1	20040921	US 2000-551161	20000414
CA 2405960	AA	20011025	CA 2000-2405960	20001019
EP 1276898	A1	20030122	EP 2000-973687	20001019
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
BR 2000017215	A	20040210	BR 2000-17215	20001019
PRAI US 2000-551161	A	20000414		
US 1999-129713P	P	19990416		
US 1999-153685P	P	19990914		
WO 2000-US28961	W	20001019		

AB Fluorescent DNA probes specific and flanking **primer** pairs are designed based on the sequence information found in the conserved terminal **3'-noncoding** region of flavivirus, e.g. nucleotides 10653-10678 of dengue virus. Fluorogenic **polymerase chain reaction** employing these **primers** and probes produce results that permit specific flavivirus identification. The assays can be both quant. and qual. Optimal assay conditions with zero background are disclosed which permit the detection of low levels of flavivirus from clin. specimens. Specifically, Dengue virus isolates from different geog. regions can be universally detected and identified by the disclosed fluorogenic **RT-PCR** assay. The fluorogenic **RT-PCR** assay readily detected viremia in sera collected from individuals ill with dengue fever.

L5 ANSWER 4 OF 7 MEDLINE on STN DUPLICATE 2
AN 97301651 MEDLINE
DN PubMed ID: 9158052
TI Rapid diagnosis of dengue viremia by reverse transcriptase-**polymerase chain reaction** using **3'-noncoding** region universal **primers**.
AU Sudiro T M; Ishiko H; Green S; Vaughn D W; Nisalak A; Kalayanarooj S; Rothman A L; Raengsakulrach B; Janus J; Kurane I; Ennis F A
CS Division of Infectious Diseases and Immunology, University of Massachusetts Medical School, Worcester 01655, USA.
NC PO1-AI-34533 (NIAID)
SO American journal of tropical medicine and hygiene, (1997 Apr) 56 (4) 424-9.

Journal code: 0370507. ISSN: 0002-9637.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199706
ED Entered STN: 19970612
Last Updated on STN: 19970612
Entered Medline: 19970602
AB A reverse transcriptase-**polymerase chain reaction** (**RT-PCR**) method was developed as a rapid diagnostic test of dengue viremia. To detect dengue viruses in serum or plasma specimens, a pair of universal **primers** was designed for use in the **RT-PCR**. Using these **primers**, the **3'-noncoding** region of dengue **virus** types 1, 2, 3, and 4 could be amplified, but not those of other flaviviruses, such as **West Nile virus**, Japanese encephalitis **virus**, and yellow fever **virus**, or the alphavirus Sindbis **virus**. The sensitivity of the **RT-PCR** assay was similar to that of a quantitative fluorescent focus assay of dengue viruses in cell culture. Combining a silica method for RNA isolation and **RT-PCR** dengue virus could be detected in a 6-hr assay. In a preliminary study using this method, we detected dengue virus in 38 of 39 plasma specimens from which dengue virus had been isolated by mosquito inoculation. We then applied this method for detecting dengue viremia to 117 plasma samples from 62 children with acute febrile illnesses in a dengue-endemic area. We detected dengue viremia in 19 of 20 samples obtained on the day of presentation, which had been confirmed as acute dengue infection by mosquito inoculation and antibody responses. The overall sensitivity of this method was 91.4% (32 of 35; 95% confidence interval [CI] = 82.2-100%). The results from testing plasma samples from febrile nondengue patients showed a specificity of 95.4% (42 of 44; 95% CI = 89.3-100%).

L5 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
AN 1996:250215 CAPLUS
DN 124:309122
TI Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus
AU Poidinger, Michael; Hall, Roy A.; Mackenzie, John S.
CS Dep. Microbiol., Univ. Queensland, Brisbane, 4072, Australia
SO Virology (1996), 218(2), 417-21
CODEN: VIRLAX; ISSN: 0042-6822
PB Academic
DT Journal
LA English
AB The Japanese encephalitis (JE) serocomplex of flaviviruses comprises 10 members, 9 of which: Alfuy (ALF); Koutango (KOU); Kokobera (KOK); Kunjin (KUN); Murray Valley encephalitis (MVE); JE; Stratford (STR); Usutu (USU); and West Nile (WN) have been isolated from Africa, southern Europe, Middle East, Asia, and Australia. The tenth member, St. Louis encephalitis (SLE) virus, is confined to North, Central, and South America. For ALF, KOK, KOU, STR, and USU, no sequence data have as yet been reported, and little mol. phylogeny has been determined for this complex as a whole. Using a rapid, one-step **RT-PCR** and universal **primers**, we have amplified and sequenced a 450-600 base pair region of the virus genome encompassing the N terminus of the nonstructural protein NS5 and the 5' end of the **3' noncoding** region, for several strains of all of these viruses, except USU and SLE viruses. These data, as well as published sequence data for other flaviviruses, were analyzed with the ClustalW and Phylip computer packages. The resultant phylogenetic data were consistent with some of the current flavivirus serol. classification, showing a close relationship between ALF and MVE viruses and between KOK and STR viruses, but suggested that KOK and STR are distantly related to the other viruses and should perhaps be reclassified in their own serocomplex. The data also confirmed the close relationship between KUN and WN viruses and showed that an isolate of KUN

virus from Sarawak may represent a "link" between these two virus species. In addition, the primary sequence data revealed a polymorphic region just downstream of the stop codon in the 3' end of the viral genomes.

L5 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 4
AN 94337023 MEDLINE
DN PubMed ID: 7520190
TI Identification of mosquito-borne flavivirus sequences using universal **primers** and reverse transcription/**polymerase chain reaction**.
AU Pierre V; Drouet M T; Deubel V
CS Unite des Arbovirus et virus des fievres hemorragiques, Institut Pasteur, Paris.
SO Research in virology, (1994 Mar-Apr) 145 (2) 93-104.
Journal code: 8907469. ISSN: 0923-2516.
CY France
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199409
ED Entered STN: 19940920
Last Updated on STN: 19960129
Entered Medline: 19940909
AB A reverse transcription/**polymerase chain reaction** (**RT/PCR**) protocol for the rapid detection and identification of flaviviruses was developed using a set of universal oligonucleotide **primers**. These **primers** correspond to sequences in the **3' non-coding** region and in the NS5 gene which are highly conserved among the mosquito-borne flaviviruses. The sequences of the resulting amplified products were analysed for dengue 1, dengue 2, dengue 3, dengue 4, Japanese encephalitis, **West Nile**, yellow fever and Zika **viruses**, and compared with the published sequences of other flaviviruses. The 291-297 nucleotides corresponding to the C-terminus of NS5 gene showed 56 to 76% similarity, whereas the **3' non -coding** region (190 to 421 nucleotides) showed only 20 to 36% similarity. Genetic classification of the Zika virus supported its traditional serological grouping. Recombinant plasmids containing the flavivirus sequences were used in a nucleic acid **hybridization** test to identify the **RT/PCR** products derived from viral RNA extracted from experimentally infected mosquitoes. The plasmids were dotted on a strip of nitrocellulose membrane and incubated with the **RT/PCR** product labelled with digoxigenin during the **PCR** step. This is a valuable method for the rapid and specific identification of mosquito-borne flaviviruses in biological specimens and for subsequent sequence analysis.

L5 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5
AN 1993:442105 CAPLUS
DN 119:42105
TI Rapid identification of flavivirus using the **polymerase chain reaction**
AU Tanaka, Mariko
CS Inst. Trop. Med., Nagasaki Univ., Nagasaki, 852, Japan
SO Journal of Virological Methods (1993), 41(3), 311-22
CODEN: JVMEDH; ISSN: 0166-0934
DT Journal
LA English
AB A rapid and accurate detection and identification system was developed for flaviviruses that makes use of reverse transcription-**polymerase chain reaction** (**RT-PCR**). A **primer** pair (YF-1 and YF-**3**), which corresponds to the highly conserved sequence from the **3' noncoding** region among flaviviruses, was useful for identification of mosquito-borne flaviviruses. Nine sets of species-specific **primer** pairs were also selected to identify and distinguish species, i.e., yellow fever, **West Nile**, Murray Valley encephalitis, Japanese encephalitis, St. Louis encephalitis, and dengue type 1 to 4

viruses. This method required only 2 h for completion using infected culture fluid, thus facilitating rapid identification of mosquito-borne flavivirus species.

L5 ANSWER 1 OF 7 MEDLINE on STN DUPLICATE 1
AN 2004065831 MEDLINE
DN PubMed ID: 14766868
TI Use of an internal positive control in a multiplex reverse transcription-**PCR** to detect **West Nile virus** RNA in mosquito pools.
AU Eisler Diane L; McNabb Alan; Jorgensen Danielle R; Isaac-Renton Judith L
CS Division of Laboratory Services, British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada.. diane.eisler@bccdc.ca
SO Journal of clinical microbiology, (2004 Feb) 42 (2) 841-3. Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF196835
EM 200404
ED Entered STN: 20040210
Last Updated on STN: 20040410
Entered Medline: 20040409
AB We report on the use of **West Nile virus** Armored RNA as an internal positive control (IPC) for the extraction and reverse transcription-**PCR** (**RT-PCR**) of RNA extracted from field-collected mosquitoes and on a multiplex real-time Taqman **RT-PCR** to simultaneously detect the **3' noncoding** region of **West Nile virus** and the **West Nile virus** NS5-2 region comprising the IPC. Mosquito pools from the province of British Columbia, Canada (n = 635), were tested in duplicate and found to be negative for **West Nile virus** and positive for the IPC. Known **West Nile virus**-positive supernatants from mosquito pools from the provinces of Alberta and Manitoba were tested in duplicate and found to be positive for both regions of the **West Nile virus** genome. The mean cycle threshold (Ct) value for the IPC in batch extraction controls +/- 2 standard deviations was found to be 36.43 +/- 1.78 cycles. IPCs of 98.4% (624) of **West Nile virus**-negative pools fell within this range, indicating the reproducibility of RNA extraction and **RT-PCR** for pools varying in mosquito genus and number. A comparison of mosquito pool genera revealed no significant genus effect on the Ct value of the IPC. The incorporation of **West Nile virus** Armored RNA as an IPC allows monitoring of RNA extraction and **RT-PCR** and detection of false-negative results due to failures in these processes or to **PCR** inhibition, respectively.

L5 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:842060 CAPLUS
DN 138:148319
TI Rapid detection of **West Nile Virus**
AU Landt, Olfert; Dehnhardt, Jasmin; Nitsche, Andreas; Milburn, Gary; Carver, Shawn D.
CS Research and Development Unit, TIB MOLBIOL Berlin, Berlin, 10829, Germany
SO Rapid Cycle Real-Time PCR: Methods and Applications--Microbiology and Food Analysis (2002), 227-234. Editor(s): Reischl, Udo; Wittwer, Carl; Cockerill, Franklin. Publisher: Springer-Verlag, Berlin, Germany. CODEN: 69DFMB; ISBN: 3-540-41881-4
DT Conference
LA English
AB **West Nile virus** (WNV) is a flavivirus endemic in Africa, the Middle East, and in South-Western Asia. The virus is a member of the Japanese encephalitis serocomplex, containing a plus-strand ssRNA genome. A few **RT-PCR** based diagnostic assays have been previously described. The amplification efficiency and detection are usually based on the TaqMan probe based real-time **PCR** assays using the genomic region for the nonstructural proteins NS3 and NS5. The developed rapid method uses a new **hybridization**

probe-based assay targeting the published **3'-noncoding** region (3NC sequences).

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2001:781171 CAPLUS
DN 135:340146
TI Flavivirus detection and quantification assay using fluorogenic **RT-PCR**
IN Houng, Huo-Shu H.; Kanesa-Thasan, Niranjan
PA U.S. Army Medical Research and Material Command, USA
SO PCT Int. Appl., 50 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001079546	A2	20011025	WO 2000-US28961	20001019
	WO 2001079546	A3	20030605		
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	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6793488	B1	20040921	US 2000-551161	20000414
	CA 2405960	AA	20011025	CA 2000-2405960	20001019
	EP 1276898	A1	20030122	EP 2000-973687	20001019
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
	BR 2000017215	A	20040210	BR 2000-17215	20001019
PRAI	US 2000-551161	A	20000414		
	US 1999-129713P	P	19990416		
	US 1999-153685P	P	19990914		
	WO 2000-US28961	W	20001019		

AB Fluorescent DNA probes specific and flanking **primer** pairs are designed based on the sequence information found in the conserved terminal **3'-noncoding** region of flavivirus, e.g. nucleotides 10653-10678 of dengue virus. Fluorogenic **polymerase chain reaction** employing these **primers** and probes produce results that permit specific flavivirus identification. The assays can be both quant. and qual. Optimal assay conditions with zero background are disclosed which permit the detection of low levels of flavivirus from clin. specimens. Specifically, Dengue virus isolates from different geog. regions can be universally detected and identified by the disclosed fluorogenic **RT-PCR** assay. The fluorogenic **RT-PCR** assay readily detected viremia in sera collected from individuals ill with dengue fever.

L5 ANSWER 4 OF 7 MEDLINE on STN DUPLICATE 2
AN 97301651 MEDLINE
DN PubMed ID: 9158052
TI Rapid diagnosis of dengue viremia by reverse transcriptase-**polymerase chain reaction** using **3'-noncoding** region universal **primers**.
AU Sudiro T M; Ishiko H; Green S; Vaughn D W; Nisalak A; Kalayanarooj S; Rothman A L; Raengsakulrach B; Janus J; Kurane I; Ennis F A
CS Division of Infectious Diseases and Immunology, University of Massachusetts Medical School, Worcester 01655, USA.
NC PO1-AI-34533 (NIAID)
SO American journal of tropical medicine and hygiene, (1997 Apr) 56 (4) 424-9.

Journal code: 0370507. ISSN: 0002-9637.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199706
ED Entered STN: 19970612
Last Updated on STN: 19970612
Entered Medline: 19970602
AB A reverse transcriptase-**polymerase chain reaction** (**RT-PCR**) method was developed as a rapid diagnostic test of dengue viremia. To detect dengue viruses in serum or plasma specimens, a pair of universal **primers** was designed for use in the **RT-PCR**. Using these **primers**, the **3'-noncoding** region of dengue **virus** types 1, 2, **3**, and 4 could be amplified, but not those of other flaviviruses, such as **West Nile virus**, Japanese encephalitis **virus**, and yellow fever **virus**, or the alphavirus Sindbis **virus**. The sensitivity of the **RT-PCR** assay was similar to that of a quantitative fluorescent focus assay of dengue viruses in cell culture. Combining a silica method for RNA isolation and **RT-PCR** dengue virus could be detected in a 6-hr assay. In a preliminary study using this method, we detected dengue virus in 38 of 39 plasma specimens from which dengue virus had been isolated by mosquito inoculation. We then applied this method for detecting dengue viremia to 117 plasma samples from 62 children with acute febrile illnesses in a dengue-endemic area. We detected dengue viremia in 19 of 20 samples obtained on the day of presentation, which had been confirmed as acute dengue infection by mosquito inoculation and antibody responses. The overall sensitivity of this method was 91.4% (32 of 35; 95% confidence interval [CI] = 82.2-100%). The results from testing plasma samples from febrile nondengue patients showed a specificity of 95.4% (42 of 44; 95% CI = 89.3-100%).

L5 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
AN 1996:250215 CAPLUS
DN 124:309122
TI Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus
AU Poidinger, Michael; Hall, Roy A.; Mackenzie, John S.
CS Dep. Microbiol., Univ. Queensland, Brisbane, 4072, Australia
SO Virology (1996), 218(2), 417-21
CODEN: VIRLAX; ISSN: 0042-6822
PB Academic
DT Journal
LA English
AB The Japanese encephalitis (JE) serocomplex of flaviviruses comprises 10 members, 9 of which: Alfuy (ALF); Koutango (KOU); Kokobera (KOK); Kunjin (KUN); Murray Valley encephalitis (MVE); JE; Stratford (STR); Usutu (USU); and West Nile (WN) have been isolated from Africa, southern Europe, Middle East, Asia, and Australia. The tenth member, St. Louis encephalitis (SLE) virus, is confined to North, Central, and South America. For ALF, KOK, KOU, STR, and USU, no sequence data have as yet been reported, and little mol. phylogeny has been determined for this complex as a whole. Using a rapid, one-step **RT-PCR** and universal **primers**, we have amplified and sequenced a 450-600 base pair region of the virus genome encompassing the N terminus of the nonstructural protein NS5 and the 5' end of the **3' noncoding** region, for several strains of all of these viruses, except USU and SLE viruses. These data, as well as published sequence data for other flaviviruses, were analyzed with the ClustalW and Phylip computer packages. The resultant phylogenetic data were consistent with some of the current flavivirus serol. classification, showing a close relationship between ALF and MVE viruses and between KOK and STR viruses, but suggested that KOK and STR are distantly related to the other viruses and should perhaps be reclassified in their own serocomplex. The data also confirmed the close relationship between KUN and WN viruses and showed that an isolate of KUN

virus from Sarawak may represent a "link" between these two virus species. In addition, the primary sequence data revealed a polymorphic region just downstream of the stop codon in the 3' end of the viral genomes.

L5 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 4
AN 94337023 MEDLINE
DN PubMed ID: 7520190
TI Identification of mosquito-borne flavivirus sequences using universal **primers** and reverse transcription/**polymerase chain reaction**.
AU Pierre V; Drouet M T; Deubel V
CS Unite des Arbovirus et virus des fievres hemorragiques, Institut Pasteur, Paris.
SO Research in virology, (1994 Mar-Apr) 145 (2) 93-104.
Journal code: 8907469. ISSN: 0923-2516.
CY France
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199409
ED Entered STN: 19940920
Last Updated on STN: 19960129
Entered Medline: 19940909
AB A reverse transcription/**polymerase chain reaction** (**RT/PCR**) protocol for the rapid detection and identification of flaviviruses was developed using a set of universal oligonucleotide **primers**. These **primers** correspond to sequences in the **3' non-coding** region and in the NS5 gene which are highly conserved among the mosquito-borne flaviviruses. The sequences of the resulting amplified products were analysed for dengue 1, dengue 2, dengue 3, dengue 4, Japanese encephalitis, **West Nile**, yellow fever and Zika **viruses**, and compared with the published sequences of other flaviviruses. The 291-297 nucleotides corresponding to the C-terminus of NS5 gene showed 56 to 76% similarity, whereas the **3' non -coding** region (190 to 421 nucleotides) showed only 20 to 36% similarity. Genetic classification of the Zika virus supported its traditional serological grouping. Recombinant plasmids containing the flavivirus sequences were used in a nucleic acid **hybridization** test to identify the **RT/PCR** products derived from viral RNA extracted from experimentally infected mosquitoes. The plasmids were dotted on a strip of nitrocellulose membrane and incubated with the **RT/PCR** product labelled with digoxigenin during the **PCR** step. This is a valuable method for the rapid and specific identification of mosquito-borne flaviviruses in biological specimens and for subsequent sequence analysis.

L5 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5
AN 1993:442105 CAPLUS
DN 119:42105
TI Rapid identification of flavivirus using the **polymerase chain reaction**
AU Tanaka, Mariko
CS Inst. Trop. Med., Nagasaki Univ., Nagasaki, 852, Japan
SO Journal of Virological Methods (1993), 41(3), 311-22
CODEN: JVMEDH; ISSN: 0166-0934
DT Journal
LA English
AB A rapid and accurate detection and identification system was developed for flaviviruses that makes use of reverse transcription-**polymerase chain reaction** (**RT-PCR**). A **primer** pair (YF-1 and YF-**3**), which corresponds to the highly conserved sequence from the **3' noncoding** region among flaviviruses, was useful for identification of mosquito-borne flaviviruses. Nine sets of species-specific **primer** pairs were also selected to identify and distinguish species, i.e., yellow fever, **West Nile**, Murray Valley encephalitis, Japanese encephalitis, St. Louis encephalitis, and dengue type 1 to 4

viruses. This method required only 2 h for completion using infected culture fluid, thus facilitating rapid identification of mosquito-borne flavivirus species.

L7 ANSWER 1 OF 11 MEDLINE on STN
AN 2002257163 MEDLINE
DN PubMed ID: 11996693
TI Phylogenetic analysis of a human isolate from the 2000 Israel **West Nile virus** epidemic.
AU Briese Thomas; Rambaut Andrew; Pathmajeyan Melissa; Bishara Jihad; Weinberger Miriam; Pitlik Silvio; Lipkin W Ian
CS Emerging Diseases Laboratory, Dept. of Neurology, Microbiology and Molecular Genetics, 3107 Gillespie Neuroscience Building, University of California at Irvine, Irvine, CA 92697-4292, USA.. tbriese@uci.edu
NC NS 29425 (NINDS)
SO Emerging infectious diseases, **(2002 May)** 8 (5) 528-31.
Journal code: 9508155. ISSN: 1080-6040.
CY United States
DT (CASE REPORTS)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF394217
EM 200206
ED Entered STN: 20020509
Last Updated on STN: 20020611
Entered Medline: 20020607
AB Specimens from a patient of the 2000 Israel **West Nile virus** epidemic were analyzed by reverse transcription-**polymerase chain reaction**. Products corresponding to E, NS3, and **NS5** sequences were amplified from cerebellar but not from cortical samples. Phylogenetic analyses indicated a closer relationship of this isolate to 1996 Romanian and 1999 Russian than to 1998-99 Israeli or 1999 New York isolates.

L7 ANSWER 2 OF 11 MEDLINE on STN
AN 2001460278 MEDLINE
DN PubMed ID: 11326014
TI Comparison of flavivirus universal **primer** pairs and development of a rapid, highly sensitive heminested reverse transcription-**PCR** assay for detection of flaviviruses targeted to a conserved region of the **NS5** gene sequences.
AU Scaramozzino N; Crance J M; Jouan A; DeBriel D A; Stoll F; Garin D
CS Unite de Virologie, Centre de Recherches du Service de Sante des Armees (CRSSA) Emile Parde, Grenoble, France.
SO Journal of clinical microbiology, **(2001 May)** 39 (5) 1922-7.
Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200108
ED Entered STN: 20010820
Last Updated on STN: 20010820
Entered Medline: 20010816
AB Arthropod-transmitted flaviviruses are responsible for considerable morbidity and mortality, causing severe encephalitic, hemorrhagic, and febrile illnesses in humans. Because there are no specific clinical symptoms for infection by a determined virus and because different arboviruses could be present in the same area, a genus diagnosis by **PCR** would be a useful first-line diagnostic method. The six published Flavivirus genus **primer** pairs localized in the NS1, NS3, **NS5**, and 3' NC regions were evaluated in terms of specificity and sensitivity with flaviviruses (including the main viruses pathogenic for humans) at a titer of 10(5) 50% tissue culture infectious doses (TCID(50)s) ml(-1) with a common identification step by agarose gel

electrophoresis. Only one **NS5 primer** pair allowed the detection of all tested flaviviruses with the sensitivity limit of 10(5) TCID(50)s ml(-1). Using a heminested **PCR** with new **primers** designed in the same region after an alignment of 30 different flaviviruses, the sensitivity of reverse transcription-**PCR** was improved and allowed the detection of about 200 infectious doses ml(-1) with all of the tick- and mosquito-borne flaviviruses tested. It was confirmed that the sequenced amplified products in the **NS5** region allowed predictability of flavivirus species by dendrogram, including the New York 99 **West Nile** strain. This technique was successfully performed with a cerebrospinal fluid sample from a patient hospitalized with **West Nile virus** encephalitis.

L7 ANSWER 4 OF 11 MEDLINE on STN
AN 94337023 MEDLINE
DN PubMed ID: 7520190
TI Identification of mosquito-borne flavivirus sequences using universal **primers** and reverse transcription/**polymerase chain reaction**.
AU Pierre V; Drouet M T; Deubel V
CS Unite des Arbovirus et virus des fievres hemorragiques, Institut Pasteur, Paris.
SO Research in virology, **(1994 Mar-Apr)** 145 (2) 93-104.
Journal code: 8907469. ISSN: 0923-2516.
CY France
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199409
ED Entered STN: 19940920
Last Updated on STN: 19960129
Entered Medline: 19940909
AB A reverse transcription/**polymerase chain reaction** (**RT/PCR**) protocol for the rapid detection and identification of flaviviruses was developed using a set of universal oligonucleotide **primers**. These **primers** correspond to sequences in the 3' non-coding region and in the **NS5** gene which are highly conserved among the mosquito-borne flaviviruses. The sequences of the resulting amplified products were analysed for dengue 1, dengue 2, dengue 3, dengue 4, Japanese encephalitis, **West Nile**, yellow fever and Zika **viruses**, and compared with the published sequences of other flaviviruses. The 291-297 nucleotides corresponding to the C-terminus of **NS5** gene showed 56 to 76% similarity, whereas the 3' non-coding region (190 to 421 nucleotides) showed only 20 to 36% similarity. Genetic classification of the Zika virus supported its traditional serological grouping. Recombinant plasmids containing the flavivirus sequences were used in a nucleic acid **hybridization** test to identify the **RT/PCR** products derived from viral RNA extracted from experimentally infected mosquitoes. The plasmids were dotted on a strip of nitrocellulose membrane and incubated with the **RT/PCR** product labelled with digoxigenin during the **PCR** step. This is a valuable method for the rapid and specific identification of mosquito-borne flaviviruses in biological specimens and for subsequent sequence analysis.

L7 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:842060 CAPLUS
DN 138:148319
TI Rapid detection of **West Nile Virus**
AU Landt, Olfert; Dehnhardt, Jasmin; Nitsche, Andreas; Milburn, Gary; Carver, Shawn D.
CS Research and Development Unit, TIB MOLBIOL Berlin, Berlin, 10829, Germany
SO Rapid Cycle Real-Time PCR: Methods and Applications--Microbiology and Food Analysis (**2002**), 227-234. Editor(s): Reischl, Udo; Wittwer, Carl; Cockerill, Franklin. Publisher: Springer-Verlag, Berlin, Germany.

CODEN: 69DFMB; ISBN: 3-540-41881-4
DT Conference
LA English
AB **West Nile virus** (WNV) is a flavivirus endemic in Africa, the Middle East, and in South-Western Asia. The virus is a member of the Japanese encephalitis serocomplex, containing a plus-strand ssRNA genome. A few **RT-PCR** based diagnostic assays have been previously described. The amplification efficiency and detection are usually based on the TaqMan probe based real-time **PCR** assays using the genomic region for the nonstructural proteins NS3 and **NS5**. The developed rapid method uses a new **hybridization** probe-based assay targeting the published 3'-noncoding region (3NC sequences).
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2000:365691 CAPLUS
DN 134:173557
TI Detection of **West Nile virus** sequences in cerebrospinal fluid
AU Briese, T.; Glass, W. G.; Lipkin, W. I.
CS Departments of Neurology, Microbiology and Molecular Genetics, Anatomy, and Neurobiology, Emerging Diseases Laboratory, University of California, Irvine, CA, 92697-4292, USA
SO Lancet (**2000**), 355(9215), 1614-1615
CODEN: LANCAO; ISSN: 0140-6736
PB Lancet Ltd.
DT Journal
LA English
AB We have established a sensitive and specific real-time **PCR** method for detection of **West Nile virus**. Anal. of specimens obtained during the 1999 New York outbreak indicated the presence of viral sequences in cerebrospinal fluid of all of four individuals with fatal outcomes, and in only one of four who survived.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1996:250215 CAPLUS
DN 124:309122
TI Molecular characterization of the Japanese encephalitis serocomplex of the flavivirus genus
AU Poidinger, Michael; Hall, Roy A.; Mackenzie, John S.
CS Dep. Microbiol., Univ. Queensland, Brisbane, 4072, Australia
SO Virology (**1996**), 218(2), 417-21
CODEN: VIRLAX; ISSN: 0042-6822
PB Academic
DT Journal
LA English
AB The Japanese encephalitis (JE) serocomplex of flaviviruses comprises 10 members, 9 of which: Alfuy (ALF); Koutango (KOU); Kokobera (KOK); Kunjin (KUN); Murray Valley encephalitis (MVE); JE; Stratford (STR); Usutu (USU); and **West Nile** (WN) have been isolated from Africa, southern Europe, Middle East, Asia, and Australia. The tenth member, St. Louis encephalitis (SLE) virus, is confined to North, Central, and South America. For ALF, KOK, KOU, STR, and USU, no sequence data have as yet been reported, and little mol. phylogeny has been determined for this complex as a whole. Using a rapid, one-step **RT-PCR** and universal **primers**, we have amplified and sequenced a 450-600 base pair region of the virus genome encompassing the N terminus of the **nonstructural** protein **NS5** and the **5'** end of the 3' noncoding region, for several strains of all of these viruses, except USU and SLE viruses. These data, as well as published sequence data for other flaviviruses, were analyzed with the ClustalW and Phylip computer packages. The resultant phylogenetic data were consistent with some of the current flavivirus serol. classification, showing a close

relationship between ALF and MVE viruses and between KOK and STR viruses, but suggested that KOK and STR are distantly related to the other viruses and should perhaps be reclassified in their own serocomplex. The data also confirmed the close relationship between KUN and WN viruses and showed that an isolate of KUN virus from Sarawak may represent a "link" between these two virus species. In addition, the primary sequence data revealed a polymorphic region just downstream of the stop codon in the 3' end of the viral genomes.

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AN 2000:384295 BIOSIS

DN PREV200000384295

TI Universal **RT-PCR** for specific and sensitive detection of flaviviruses.

AU Scaramozzino, N. [Reprint author]; Crance, J. M. [Reprint author]; Rothlisberger, C. [Reprint author]; Gratier, D. [Reprint author]; Blancquaert, H. [Reprint author]; Guimet, J. [Reprint author]; DeBriel, D.; Jouan, A. [Reprint author]; Garin, D. [Reprint author]

CS CRSSA Emile Parde, Grenoble, France

SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 140-141. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology. Los Angeles, California, USA. May 21-25, 2000. American Society for Microbiology.
ISSN: 1060-2011.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 6 Sep 2000
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